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RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/10/051,311A

TIME: 10:30:16

Input Set : A:\seqlist0652_2290001.txt

Output Set: N:\CRF3\07102002\J051311A.raw

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3 <110> APPLICANT: Boehringer Ingelheim International GmbH
5 <120> TITLE OF INVENTION: Method for identifying compounds that modulate sister
6   chromatid separation
8 <130> FILE REFERENCE: 0652.2290001
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/051,311A
C--> 11 <141> CURRENT FILING DATE: 2002-06-20
13 <150> PRIOR APPLICATION NUMBER: EP 01 101 252.3
14 <151> PRIOR FILING DATE: 2001-01-19
16 <150> PRIOR APPLICATION NUMBER: US 60/297,440
17 <151> PRIOR FILING DATE: 2001-06-13
19 <160> NUMBER OF SEQ ID NOS: 13
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6668
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 <222> LOCATION: (1)..(144)
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34 <222> LOCATION: (145)..(6507)
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45 ccttttccct agctctccgg tgct atg agg agc ttc aaa aga gtc aac ttt 171
46                               Met Arg Ser Phe Lys Arg Val Asn Phe
47                               1           5
49 ggg act ctg cta agc agc cag aag gag gct gaa gag ttg ctg ccc gac 219
50 Gly Thr Leu Leu Ser Ser Gln Lys Glu Ala Glu Glu Leu Leu Pro Asp
51 10                               15           20           25
53 ttg aag gag ttc ctg tcc aac cct cca gct ggt ttt ccc agc agc cga 267
54 Leu Lys Glu Phe Leu Ser Asn Pro Pro Ala Gly Phe Pro Ser Ser Arg
55                               30           35           40
57 tct gat gct gag agg aga caa gct tgt gat gcc atc ctg agg gct tgc 315
58 Ser Asp Ala Glu Arg Arg Gln Ala Cys Asp Ala Ile Leu Arg Ala Cys
59                               45           50           55
61 aac cag cag ctg act gct aag cta gct tgc cct agg cat ctg ggg agc 363
62 Asn Gln Gln Leu Thr Ala Lys Leu Ala Cys Pro Arg His Leu Gly Ser
63                               60           65           70

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65 ctg ctg gag ctg gca gag ctg gcc tgt gat ggc tac tta gtg tct acc 411
66 Leu Leu Glu Leu Ala Glu Leu Ala Cys Asp Gly Tyr Leu Val Ser Thr
67 75 80 85
70 cca cag cgt cct ccc ctc tac ctg gaa cga att ctc ttt gtc tta ctg 459
71 Pro Gln Arg Pro Pro Leu Tyr Leu Glu Arg Ile Leu Phe Val Leu Leu
72 90 95 100 105
74 cgg aat gct gct gca caa gga agc cca gag gtc aca ctc cgc ctt gct 507
75 Arg Asn Ala Ala Ala Gln Gly Ser Pro Glu Val Thr Leu Arg Leu Ala
76 110 115 120
78 cag ccc ctc cat gcc tgc ttg gtg cag tgc tct cgc gag gct gct ccc 555
79 Gln Pro Leu His Ala Cys Leu Val Gln Cys Ser Arg Glu Ala Ala Pro
80 125 130 135
82 cag gac tat gag gcc gtg gct cgg ggc agc ttt tct ctg ctt tgg aag 603
83 Gln Asp Tyr Glu Ala Val Ala Arg Gly Ser Phe Ser Leu Leu Trp Lys
84 140 145 150
86 ggg gca gaa gcc ctg ttg gaa cgg cga gct gca ttt gca gct cgg ctg 651
87 Gly Ala Glu Ala Leu Leu Glu Arg Arg Ala Ala Phe Ala Ala Arg Leu
88 155 160 165
90 aag gcc ttg agc ttc cta gta ctc ttg gag gat gaa agt acc cct tgt 699
91 Lys Ala Leu Ser Phe Leu Val Leu Leu Glu Asp Glu Ser Thr Pro Cys
92 170 175 180 185
94 gag gtt cct cac ttt gct tct cca aca gcc tgt cga gcg gta gct gcc 747
95 Glu Val Pro His Phe Ala Ser Pro Thr Ala Cys Arg Ala Val Ala Ala
96 190 195 200
98 cat cag cta ttt gat gcc agt ggc cat ggt cta aat gaa gca gat gct 795
99 His Gln Leu Phe Asp Ala Ser Gly His Gly Leu Asn Glu Ala Asp Ala
100 205 210 215
102 gat ttc cta gat gac ctg ctc tcc agg cac gtg atc aga gcc ttg gtg 843
103 Asp Phe Leu Asp Asp Leu Leu Ser Arg His Val Ile Arg Ala Leu Val
104 220 225 230
106 ggt gag aga ggg agc tct tct ggg ctt ctt tct ccc cag agg gcc ctc 891
107 Gly Glu Arg Gly Ser Ser Ser Gly Leu Leu Ser Pro Gln Arg Ala Leu
108 235 240 245
110 tgc ctc ttg gag ctc acc ttg gaa cac tgc cgt cgc ttt tgc tgg agc 939
111 Cys Leu Leu Glu Leu Thr Leu Glu His Cys Arg Arg Phe Cys Trp Ser
112 250 255 260 265
114 cgc cac cat gac aaa gcc atc agc gca gtg gag aag gct cac agt tac 987
115 Arg His His Asp Lys Ala Ile Ser Ala Val Glu Lys Ala His Ser Tyr
116 270 275 280
118 cta agg aac acc aat cta gcc cct agc ctt cag cta tgt cag ctg ggg 1035
119 Leu Arg Asn Thr Asn Leu Ala Pro Ser Leu Gln Leu Cys Gln Leu Gly
120 285 290 295
122 gtt aag ctg ctg cag gtt ggg gag gaa gga cct cag gca gtg gcc aag 1083
123 Val Lys Leu Leu Gln Val Gly Glu Glu Gly Pro Gln Ala Val Ala Lys
124 300 305 310
126 ctt ctg atc aag gca tca gct gtc ctg agc aag agt atg gag gca cca 1131
127 Leu Leu Ile Lys Ala Ser Ala Val Leu Ser Lys Ser Met Glu Ala Pro
128 315 320 325
130 tca ccc cca ctt cgg gca ttg tat gag agc tgc cag ttc ttc ctt tca 1179

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131 Ser Pro Pro Leu Arg Ala Leu Tyr Glu Ser Cys Gln Phe Phe Leu Ser
132 330          335          340          345
134 ggc ctg gaa cga ggc acc aag agg cgc tat aga ctt gat gcc att ctg 1227
135 Gly Leu Glu Arg Gly Thr Lys Arg Arg Tyr Arg Leu Asp Ala Ile Leu
136          350          355          360
138 agc ctc ttt gct ttt ctt gga ggg tac tgc tct ctt ctg cag cag ctg 1275
139 Ser Leu Phe Ala Phe Leu Gly Gly Tyr Cys Ser Leu Leu Gln Gln Leu
140          365          370          375
142 cgg gat gat ggt gtg tat ggg ggc tcc tcc aag caa cag cag tct ttt 1323
143 Arg Asp Asp Gly Val Tyr Gly Gly Ser Ser Lys Gln Gln Gln Ser Phe
144          380          385          390
146 ctt cag atg tac ttt cag gga ctt cac ctc tac act gtg gtg gtt tat 1371
147 Leu Gln Met Tyr Phe Gln Gly Leu His Leu Tyr Thr Val Val Val Tyr
148          395          400          405
150 gac ttt gcc caa ggc tgt cag ata gtt gat ttg gct gac ctg acc caa 1419
151 Asp Phe Ala Gln Gly Cys Gln Ile Val Asp Leu Ala Asp Leu Thr Gln
152 410          415          420          425
154 cta gtg gac agt tgt aaa tct acc gtt gtc tgg atg ctg gag gcc tta 1467
155 Leu Val Asp Ser Cys Lys Ser Thr Val Val Trp Met Leu Glu Ala Leu
156          430          435          440
158 gag ggc ctg tcg ggc caa gag ctg acg gac cac atg ggg atg acc gct 1515
159 Glu Gly Leu Ser Gly Gln Glu Leu Thr Asp His Met Gly Met Thr Ala
160          445          450          455
162 tct tac acc agt aat ttg gcc tac agc ttc tat agt cac aag ctc tat 1563
163 Ser Tyr Thr Ser Asn Leu Ala Tyr Ser Phe Tyr Ser His Lys Leu Tyr
164          460          465          470
166 gcc gag gcc tgt gcc atc tct gag ccg ctc tgt cag cac ctg ggt ttg 1611
167 Ala Glu Ala Cys Ala Ile Ser Glu Pro Leu Cys Gln His Leu Gly Leu
168          475          480          485
170 gtg aag cca ggc act tat ccc gag gtg cct cct gag aag ttg cac agg 1659
171 Val Lys Pro Gly Thr Tyr Pro Glu Val Pro Pro Glu Lys Leu His Arg
172 490          495          500          505
174 tgc ttc cgg cta caa gta gag agt ttg aag aaa ctg ggt aaa cag gcc 1707
175 Cys Phe Arg Leu Gln Val Glu Ser Leu Lys Lys Leu Gly Lys Gln Ala
176          510          515          520
178 cag ggc tgc aag atg gtg att ttg tgg ctg gca gcc ctg caa ccc tgt 1755
179 Gln Gly Cys Lys Met Val Ile Leu Trp Leu Ala Ala Leu Gln Pro Cys
180          525          530          535
182 agc cct gaa cac atg gct gag cca gtc act ttc tgg gtt cgg gtc aag 1803
183 Ser Pro Glu His Met Ala Glu Pro Val Thr Phe Trp Val Arg Val Lys
184          540          545          550
186 atg gat gcg gcc agg gct gga gac aag gag cta cag cta aag act ctg 1851
187 Met Asp Ala Ala Arg Ala Gly Asp Lys Glu Leu Gln Leu Lys Thr Leu
188          555          560          565
190 cga gac agc ctc agt ggc tgg gac ccg gag acc ctg gcc ctc ctg ctg 1899
192 Arg Asp Ser Leu Ser Gly Trp Asp Pro Glu Thr Leu Ala Leu Leu Leu
193 570          575          580          585
196 agg gag gag ctg cag gcc tac aag gcg gtg cgg gcc gac act gga cag 1947
197 Arg Glu Glu Leu Gln Ala Tyr Lys Ala Val Arg Ala Asp Thr Gly Gln

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198          590          595          600
200 gaa cgc ttc aac atc atc tgt gac ctc ctg gag ctg agc ccc gag gag 1995
201 Glu Arg Phe Asn Ile Ile Cys Asp Leu Leu Glu Leu Ser Pro Glu Glu
202          605          610          615
204 aca cca gcc ggg gcc tgg gca cga gcc acc cac ctg gta gaa ctg gct 2043
205 Thr Pro Ala Gly Ala Trp Ala Arg Ala Thr His Leu Val Glu Leu Ala
206          620          625          630
208 cag gtg ctc tgc tac cac gac ttt acg cag cag acc aac tgc tct gct 2091
209 Gln Val Leu Cys Tyr His Asp Phe Thr Gln Gln Thr Asn Cys Ser Ala
210          635          640          645
212 ctg gat gct atc cgg gaa gcc ctg cag ctt ctg gac tct gtg agg cct 2139
213 Leu Asp Ala Ile Arg Glu Ala Leu Gln Leu Leu Asp Ser Val Arg Pro
214 650          655          660          665
216 gag gcc cag gcc aga gat cag ctt ctg gac gat aaa gca cag gcc ttg 2187
217 Glu Ala Gln Ala Arg Asp Gln Leu Leu Asp Asp Lys Ala Gln Ala Leu
218          670          675          680
220 ctg tgg ctt tac atc tgt act ctg gaa gcc aaa ata cag gaa ggt atc 2235
221 Leu Trp Leu Tyr Ile Cys Thr Leu Glu Ala Lys Ile Gln Glu Gly Ile
222          685          690          695
224 gag cgg gat cgg aga gcc cag gcc cct ggt aac ttg gag gaa ttt gaa 2283
225 Glu Arg Asp Arg Arg Ala Gln Ala Pro Gly Asn Leu Glu Glu Phe Glu
226          700          705          710
228 gtc aat gac ctg aac tat gaa gat aaa ctc cag gaa gat cgt ttc cta 2331
229 Val Asn Asp Leu Asn Tyr Glu Asp Lys Leu Gln Glu Asp Arg Phe Leu
230          715          720          725
232 tac agt aac att gcc ttc aac ctg gct gca gat gct gct cag tcc aaa 2379
233 Tyr Ser Asn Ile Ala Phe Asn Leu Ala Ala Asp Ala Ala Gln Ser Lys
234 730          735          740          745
236 tgc ctg gac caa gcc ctg gcc ctg tgg aag gag ctg ctt aca aag ggg 2427
237 Cys Leu Asp Gln Ala Leu Ala Leu Trp Lys Glu Leu Leu Thr Lys Gly
238          750          755          760
240 cag gcc cca gct gta cgg tgt ctc cag cag aca gca gcc tca ctg cag 2475
241 Gln Ala Pro Ala Val Arg Cys Leu Gln Gln Thr Ala Ala Ser Leu Gln
242          765          770          775
244 atc cta gca gcc ctc tac cag ctg gtg gca aag ccc atg cag gct ctg 2523
245 Ile Leu Ala Ala Leu Tyr Gln Leu Val Ala Lys Pro Met Gln Ala Leu
246          780          785          790
248 gag gtc ctc ctg ctg cta cgg att gtc tct gag aga ctg aag gac cac 2571
249 Glu Val Leu Leu Leu Leu Arg Ile Val Ser Glu Arg Leu Lys Asp His
250          795          800          805
252 tcg aag gca gct ggc tcc tcc tgc cac atc acc cag ctc ctc ctg acc 2619
253 Ser Lys Ala Ala Gly Ser Ser Cys His Ile Thr Gln Leu Leu Leu Thr
254 810          815          820          825
257 ctc ggc tgt ccc agc tat gcc cag tta cac ctg gaa gag gca gca tcg 2667
258 Leu Gly Cys Pro Ser Tyr Ala Gln Leu His Leu Glu Glu Ala Ala Ser
259          830          835          840
261 agc ctg aag cat ctc gat cag act act gac aca tac ctg ctc ctt tcc 2715
262 Ser Leu Lys His Leu Asp Gln Thr Thr Asp Thr Tyr Leu Leu Leu Ser
263          845          850          855

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265 ctg acc tgt gat ctg ctt cga agt caa ctc tac tgg act cac cag aag 2763
266 Leu Thr Cys Asp Leu Leu Arg Ser Gln Leu Tyr Trp Thr His Gln Lys
267      860      865      870
269 gtg acc aag ggt gtc tct ctg ctg ctg tct gtg ctt cgg gat cct gcc 2811
270 Val Thr Lys Gly Val Ser Leu Leu Leu Ser Val Leu Arg Asp Pro Ala
271      875      880      885
273 ctc cag aag tcc tcc aag gct tgg tac ttg ctg cgt gtc cag gtc ctg 2859
274 Leu Gln Lys Ser Ser Lys Ala Trp Tyr Leu Leu Arg Val Gln Val Leu
275 890      895      900      905
277 cag ctg gtg gca gct tac ctt agc ctc ccg tca aac aac ctc tca cac 2907
278 Gln Leu Val Ala Ala Tyr Leu Ser Leu Pro Ser Asn Asn Leu Ser His
279      910      915      920
281 tcc ctg tgg gag cag ctc tgt gcc caa ggc tgg cag aca cct gag ata 2955
282 Ser Leu Trp Glu Gln Leu Cys Ala Gln Gly Trp Gln Thr Pro Glu Ile
283      925      930      935
285 gct ctc ata gac tcc cat aag ctc ctc cga agc atc atc ctc ctg ctg 3003
286 Ala Leu Ile Asp Ser His Lys Leu Leu Arg Ser Ile Ile Leu Leu Leu
287      940      945      950
289 atg ggc agt gac att ctc tca act cag aaa gca gct gtg gag aca tcg 3051
290 Met Gly Ser Asp Ile Leu Ser Thr Gln Lys Ala Ala Val Glu Thr Ser
291      955      960      965
293 ttt ttg gac tat ggt gaa aat ctg gta caa aaa tgg cag gtt ctt tca 3099
294 Phe Leu Asp Tyr Gly Glu Asn Leu Val Gln Lys Trp Gln Val Leu Ser
295 970      975      980      985
297 gag gtg ctg agc tgc tca gag aag ctg gtc tgc cac ctg ggc cgc ctg 3147
298 Glu Val Leu Ser Cys Ser Glu Lys Leu Val Cys His Leu Gly Arg Leu
299      990      995      1000
301 ggt agt gtg agt gaa gcc aag gcc ttt tgc ttg gag gcc cta aaa ctt 3195
302 Gly Ser Val Ser Glu Ala Lys Ala Phe Cys Leu Glu Ala Leu Lys Leu
303      1005      1010      1015
305 aca aca aag ctg cag ata cca cgc cag tgt gcc ctg ttc ctg gtg ctg 3243
306 Thr Thr Lys Leu Gln Ile Pro Arg Gln Cys Ala Leu Phe Leu Val Leu
307      1020      1025      1030
309 aag ggc gag ctg gag ctg gcc cgc aat gac att gat ctc tgt cag tcg 3291
310 Lys Gly Glu Leu Glu Leu Ala Arg Asn Asp Ile Asp Leu Cys Gln Ser
311      1035      1040      1045
313 gac ctg cag cag gtt ctg ttc ttg ctt gag tct tgc aca gag ttt ggt 3339
314 Asp Leu Gln Gln Val Leu Phe Leu Leu Glu Ser Cys Thr Glu Phe Gly
315 1050      1055      1060      1065
318 ggg gtg act cag cac ctg gac tct gtg aag aag gtc cac ctg cag aag 3387
319 Gly Val Thr Gln His Leu Asp Ser Val Lys Lys Val His Leu Gln Lys
320      1070      1075      1080
322 ggg aag cag cag gcc cag gtc ccc tgt cct cca cag ctc cca gag gag 3435
323 Gly Lys Gln Gln Ala Gln Val Pro Cys Pro Pro Gln Leu Pro Glu Glu
324      1085      1090      1095
326 gag ctc ttc cta aga ggc cct gct cta gag ctg gtg gcc act gtg gcc 3483
327 Glu Leu Phe Leu Arg Gly Pro Ala Leu Glu Leu Val Ala Thr Val Ala
328      1100      1105      1110
330 aag gag cct ggc ccc ata gca cct tct aca aac tcc tcc cca gtc ttg 3531

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13